RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/829,504_
Source: _1FWO_
Date Processed by STIC: _4/30/04_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221
Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 4.1 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
    <u>http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm</u>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<u><http://www.uspto.gov/ebc/efs/downloads/documents.htm></u> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/829,504_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ___ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ___ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ___ Misaligned Amino Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use **space characters**, instead.

4 ___ Non-ASCII

The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5 ___ Variable Length

Sequence(s) ___ contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ___ PatentIn 2.0 "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) ___. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 ___ Skipped Sequences (OLD RULES)

Sequence(s) ___ missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8 ___ Skipped Sequences (NEW RULES)

Sequence(s) _38-49_ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ___ Use of n's or Xaa's (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ___ Invalid <213> Response

Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

11 ___ Use of <220>

Sequence(s) ___ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ___ PatentIn 2.0 "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ___ Misuse of n/Xaa

"n" can only represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>

IFWO

RAW SEQUENCE LISTING   DATE: 04/30/2004
PATENT APPLICATION: US/10/829,504   TIME: 15:26:36

       Input Set : A:\23239-558A.ST25.txt
       Output Set: N:\CRF4\04122004\J829504.raw

    3 <110> APPLICANT: Epstein, David
    4   Stanton, Martin
    5   DeSouza, Errol
    6   Wilson, Chuck
    7   Grate, Dilara
    8   McCauley, Tom
    9   Diener, John
   11 <120> TITLE OF INVENTION: Stabilized Aptamers to Platelet Derived Growth Factor and
Their
   12   Use as Oncology Therapeutics
   14 <130> FILE REFERENCE: 23239-558A (ARC-58A)
C--> 16 <140> CURRENT APPLICATION NUMBER: US/10/829,504
   17 <141> CURRENT FILING DATE: 2004-04-21
   19 <160> NUMBER OF SEQ ID NOS: 98
   21 <170> SOFTWARE: PatentIn version 3.2

ERRORED SEQUENCES

     835 <210> SEQ ID NO: 38
     836 <211> LENGTH: 0
     837 <212> TYPE: DNA
C--> 838 <213> ORGANISM: Artificial:aptamer
W--> 840 <220> FEATURE:
W--> 840 <223> OTHER INFORMATION:
W--> 840 <400> 38
E--> 841 000
     844 <210> SEQ ID NO: 39
     845 <211> LENGTH: 0
     846 <212> TYPE: DNA
C--> 847 <213> ORGANISM: Artificial:aptamer
W--> 849 <220> FEATURE:
W--> 849 <223> OTHER INFORMATION:
W--> 849 <400> 39
E--> 850 000
     853 <210> SEQ ID NO: 40
     854 <211> LENGTH: 0
     855 <212> TYPE: DNA
C--> 856 <213> ORGANISM: Artificial:aptamer
W--> 858 <220> FEATURE:
W--> 858 <223> OTHER INFORMATION:
W--> 858 <400> 40
E--> 859 000
     862 <210> SEQ ID NO: 41

[Handwritten annotations: "delete all these lines", "delete", "delete", "Does Not Comply Corrected Diskette Needed", "If this is an intentionally skipped sequence, show only delete <210> 38 <400> 38 000 (see item 8 on Error Summary Sheet)"]

RAW SEQUENCE LISTING   DATE: 04/30/2004
PATENT APPLICATION: US/10/829,504   TIME: 15:26:36

        Input Set : A:\23239-558A.ST25.txt
        Output Set: N:\CRF4\04122004\J829504.raw

        863 <211> LENGTH: 0
        864 <212> TYPE: DNA
C--> 865 <213> ORGANISM: Artificial:aptamer   *delete*
W--> 867 <220> FEATURE:
W--> 867 <223> OTHER INFORMATION:
W--> 867 <400> 41
E--> 868 000   3

        871 <210> SEQ ID NO: 42
        872 <211> LENGTH: 0
        873 <212> TYPE: DNA
C--> 874 <213> ORGANISM: Artificial:aptamer   *delete*
W--> 876 <220> FEATURE:
W--> 876 <223> OTHER INFORMATION:
W--> 876 <400> 42
E--> 877 000   3

        880 <210> SEQ ID NO: 43
        881 <211> LENGTH: 0
        882 <212> TYPE: DNA
C--> 883 <213> ORGANISM: Artificial:aptamer   *delete*
W--> 885 <220> FEATURE:
W--> 885 <223> OTHER INFORMATION:
W--> 885 <400> 43
E--> 886 000   3

        889 <210> SEQ ID NO: 44
        890 <211> LENGTH: 0
        891 <212> TYPE: DNA
C--> 892 <213> ORGANISM: Artificial:aptamer   *delete*
W--> 894 <220> FEATURE:
W--> 894 <223> OTHER INFORMATION:
W--> 894 <400> 44
E--> 895 000   3

        898 <210> SEQ ID NO: 45
        899 <211> LENGTH: 0
        900 <212> TYPE: DNA
C--> 901 <213> ORGANISM: Artificial:aptamer   *delete*
W--> 903 <220> FEATURE:
W--> 903 <223> OTHER INFORMATION:
W--> 903 <400> 45
E--> 904 000   3

        907 <210> SEQ ID NO: 46
        908 <211> LENGTH: 0
        909 <212> TYPE: DNA
C--> 910 <213> ORGANISM: Artificial:aptamer   *delete*
W--> 912 <220> FEATURE:
W--> 912 <223> OTHER INFORMATION:
W--> 912 <400> 46
E--> 913 000   3

        916 <210> SEQ ID NO: 47
        917 <211> LENGTH: 0   *delete*

RAW SEQUENCE LISTING   DATE: 04/30/2004
PATENT APPLICATION: US/10/829,504   TIME: 15:26:36

Input Set : **A:\23239-558A.ST25.txt**
Output Set: **N:\CRF4\04122004\J829504.raw**

```
         918 <212> TYPE: DNA
C-->     919 <213> ORGANISM: Artificial:aptamer     delete
W-->     921 <220> FEATURE:
W-->     921 <223> OTHER INFORMATION:
W-->     921 <400> 47
E-->     922 000
         925 <210> SEQ ID NO: 48
         926 <211> LENGTH: 0
         927 <212> TYPE: DNA
C-->     928 <213> ORGANISM: Artificial:aptamer     delete
W-->     930 <220> FEATURE:
W-->     930 <223> OTHER INFORMATION:
W-->     930 <400> 48
E-->     931 000
         934 <210> SEQ ID NO: 49
         935 <211> LENGTH: 0
         936 <212> TYPE: DNA
C-->     937 <213> ORGANISM: Artificial:aptamer     delete
W-->     939 <220> FEATURE:
W-->     939 <223> OTHER INFORMATION:
W-->     939 <400> 49
E-->     940 000
```

see p. 4 for more errors

```
<210>   1
<211>   9
<212>   DNA
<213>   Artificial aptamer
<220>
<223>
<220>
<221>   modified_base
<222>   (6)..(6)
<223>   2'-Fluoro-Uracil

<220>
<221>   modified_base
<222>   (6)..(6)
<223>   2'-Fluoro-Uracil

<220>
<221>   modified_base
<222>   (8)..(8)
<223>   2'-Fluoro-Cytosine

<220>
<221>   modified_base
<222>   (9)..(9)
<223>   gm

<400>   1
caggcuacg
```

delete colon ":"

do not show explanation for Artificial Sequence on <213> line. Insert a <220>, a <223>, and move explanation to <223> line.

Explanation of Artificial Sequence must give source of genetic material.

delete - already shown above

This error appears throughout Sequence Listing.

FYI

Use of n and/or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

Input Set : **A:\23239-558A.ST25.txt**
Output Set: **N:\CRF4\04122004\J829504.raw**

L:16 M:270 C: Current Application Number differs, Replaced Current Application Number
L:26 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:56 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:91 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:116 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:156 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:191 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6
L:216 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L:326 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:328 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:8, <213>
ORGANISM:Artificial Sequence
L:328 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:8, <213>
ORGANISM:Artificial Sequence
L:328 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:328
L:335 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:445 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:545 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
L:547 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:11, <213>
ORGANISM:Artificial Sequence
L:547 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:11, <213>
ORGANISM:Artificial Sequence
L:547 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:547
L:554 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12
L:569 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:13
L:584 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14
L:599 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15
L:614 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16
L:629 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:17
L:644 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:18
L:659 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:19
L:674 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:20
L:676 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:20, <213>
ORGANISM:Artificial Sequence
L:676 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:20, <213>
ORGANISM:Artificial Sequence
L:676 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:20,Line#:676
L:683 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:21
L:685 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:21, <213>
ORGANISM:Artificial Sequence
L:685 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:21, <213>
ORGANISM:Artificial Sequence
L:685 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:21,Line#:685
L:692 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:22
L:694 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:22, <213>
ORGANISM:Artificial Sequence
L:694 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:22, <213>
ORGANISM:Artificial Sequence
L:694 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:22,Line#:694
L:703 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:23
L:705 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:23, <213>
ORGANISM:Artificial Sequence
L:705 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:23, <213>
ORGANISM:Artificial Sequence

L:705 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:23,Line#:705
L:712 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:24
L:714 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:24, <213>
ORGANISM:Artificial Sequence
L:714 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:24, <213>
ORGANISM:Artificial Sequence
L:714 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:24,Line#:714
L:721 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:25
L:723 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:25, <213>
ORGANISM:Artificial Sequence

VERIFICATION SUMMARY   DATE: 04/30/2004
PATENT APPLICATION: **US/10/829,504**   TIME: 15:26:37

Input Set : **A:\23239-558A.ST25.txt**
Output Set: **N:\CRF4\04122004\J829504.raw**

L:723 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:25, <213>
ORGANISM:Artificial Sequence
L:723 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:25,Line#:723
L:730 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:26
L:732 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:26, <213>
ORGANISM:Artificial Sequence
L:732 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:26, <213>
ORGANISM:Artificial Sequence
L:732 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:26,Line#:732
L:739 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:27
L:741 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:27, <213>
ORGANISM:Artificial Sequence
L:741 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:27, <213>
ORGANISM:Artificial Sequence
L:741 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:27,Line#:741
L:748 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:28
L:750 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:28, <213>
ORGANISM:Artificial Sequence
L:750 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:28, <213>
ORGANISM:Artificial Sequence
L:750 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:28,Line#:750
L:757 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:29
L:759 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:29, <213>
ORGANISM:Artificial Sequence
L:759 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:29, <213>
ORGANISM:Artificial Sequence
L:759 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:29,Line#:759
L:766 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:30
L:768 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:30, <213>
ORGANISM:Artificial Sequence
L:768 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:30, <213>
ORGANISM:Artificial Sequence
L:768 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:30,Line#:768
L:775 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:31
L:777 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:31, <213>
ORGANISM:Artificial Sequence
L:777 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:31, <213>
ORGANISM:Artificial Sequence
L:777 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:31,Line#:777
L:784 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:32
L:786 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:32, <213>
ORGANISM:Artificial Sequence
L:786 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:32, <213>
ORGANISM:Artificial Sequence
L:786 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:32,Line#:786
L:793 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:33
L:795 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:33, <213>
ORGANISM:Artificial Sequence
L:795 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:33, <213>
ORGANISM:Artificial Sequence
L:795 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:33,Line#:795
L:802 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:34
L:804 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:34, <213>

```
ORGANISM:Artificial Sequence
L:804 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:34, <213>
ORGANISM:Artificial Sequence
L:811 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:35
L:820 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:36
L:829 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:37
L:838 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:38
L:841 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:841 M:301 E: (44) No Sequence Data was Shown, SEQ ID:38
L:847 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:39
L:850 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:850 M:301 E: (44) No Sequence Data was Shown, SEQ ID:39
L:856 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:40
L:859 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:859 M:301 E: (44) No Sequence Data was Shown, SEQ ID:40
```

Input Set : **A:\23239-558A.ST25.txt**
Output Set: **N:\CRF4\04122004\J829504.raw**

L:865 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:41
L:868 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:868 M:301 E: (44) No Sequence Data was Shown, SEQ ID:41
L:874 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:42
L:877 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:877 M:301 E: (44) No Sequence Data was Shown, SEQ ID:42
L:883 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:43
L:886 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:886 M:301 E: (44) No Sequence Data was Shown, SEQ ID:43
L:892 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:44
L:895 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:895 M:301 E: (44) No Sequence Data was Shown, SEQ ID:44
L:901 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:45
L:904 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:904 M:301 E: (44) No Sequence Data was Shown, SEQ ID:45
L:910 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:46
L:913 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:913 M:301 E: (44) No Sequence Data was Shown, SEQ ID:46
L:919 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:47
L:922 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:922 M:301 E: (44) No Sequence Data was Shown, SEQ ID:47
L:928 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:48
L:931 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:931 M:301 E: (44) No Sequence Data was Shown, SEQ ID:48
L:937 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:49
L:940 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:940 M:301 E: (44) No Sequence Data was Shown, SEQ ID:49
L:946 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:50
L:955 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50 after pos.:0
L:972 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51 after pos.:0
L:989 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:52 after pos.:0
L:1863 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:91 after pos.:0
M:341 Repeated in SeqNo=91